

BLASTP 2.2.20+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: YSX40DNX016

Database: Protein sequences derived from the Patent division of GenBank

644,914 sequences; 121,161,582 total letters

Query=

Length=16

Sequences producing significant alignments:		Score (Bits)	E Value
gb AAA02142.1	Sequence 1 from Patent US 4885357	20.2	0.45
gb AAA55740.1	Sequence 14 from Patent EP 0330191	18.9	1.1
gb AAA53711.1	Sequence 3 from Patent WO 9000563	18.9	1.1
gb AAA56309.1	Sequence 7 from Patent EP 0196864	18.0	2.0
gb AAA54420.1	Sequence 14 from Patent WO 8806628 >gb AAA5600...	18.0	2.0
gb AAA54815.1	Sequence 19 from Patent WO 8607383	17.6	2.6
gb AAA53695.1	Sequence 2 from Patent WO 9004640	17.2	3.5
gb AAA54560.1	Sequence 2 from Patent WO 8805081 >gb AAA56055...	16.8	4.7
gb AAA54001.1	Sequence 2 from Patent WO 8906283 >gb AAA54156...	15.9	8.5
gb AAA00924.1	Sequence 1 from Patent US 4657891	15.9	8.5

ALIGNMENTS

>gb|AAA02142.1| Sequence 1 from Patent US 4885357
Length=21

Score = 20.2 bits (40), Expect = 0.45
Identities = 6/6 (100%), Positives = 6/6 (100%), Gaps = 0/6 (0%)

```
Query  10  LLALLA  15
          LLALLA
Sbjct  8   LLALLA  13
```

Score = 16.3 bits (31), Expect = 6.4
Identities = 7/11 (63%), Positives = 7/11 (63%), Gaps = 2/11 (18%)

```
Query  5   LLPAVLLALLA  15
          LL   LLAL  A
Sbjct  8   LLA--LLALFA  16
```

>gb|AAA55740.1| Sequence 14 from Patent EP 0330191
Length=27

Score = 18.9 bits (37), Expect = 1.1
Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 1/9 (11%)

```
Query  5   LLPAVLLAL  13
          LLP +LLAL
```

Sbjct 9 LLP-LLLAL 16

Score = 15.1 bits (28), Expect = 15
Identities = 6/10 (60%), Positives = 6/10 (60%), Gaps = 3/10 (30%)

Query 5 LLPAVLLALL 14
LL LL LL
Sbjct 7 LL---LLPLL 13

>gb|AAA53711.1| Sequence 3 from Patent WO 9000563
Length=99

Score = 18.9 bits (37), Expect = 1.1
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 2 AVALLPA 8
AVALL A
Sbjct 6 AVALLAA 12

Score = 15.1 bits (28), Expect = 15
Identities = 6/8 (75%), Positives = 6/8 (75%), Gaps = 2/8 (25%)

Query 8 AVLLALLA 15
AV ALLA
Sbjct 6 AV--ALLA 11

>gb|AAA56309.1| Sequence 7 from Patent EP 0196864
Length=77

Score = 18.0 bits (35), Expect = 2.0
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 2/10 (20%)

Query 2 AVALLPAVLL 11
A+ALLP LL
Sbjct 7 ALALLP--LL 14

Score = 14.6 bits (27), Expect = 21
Identities = 4/4 (100%), Positives = 4/4 (100%), Gaps = 0/4 (0%)

Query 11 LALL 14
LALL
Sbjct 8 LALL 11

Score = 9.1 bits (14), Expect = 943
Identities = 2/2 (100%), Positives = 2/2 (100%), Gaps = 0/2 (0%)

Query 13 LL 14
LL
Sbjct 69 LL 70

>gb|AAA54420.1| Sequence 14 from Patent WO 8806628
gb|AAA56005.1| Sequence 5 from Patent EP 0281363
Length=91

Score = 18.0 bits (35), Expect = 2.0
 Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 2/10 (20%)

Query 2 AVALLPAVLL 11
 A+ALLP LL
 Sbjct 7 ALALLP--LL 14

Score = 14.6 bits (27), Expect = 21
 Identities = 4/4 (100%), Positives = 4/4 (100%), Gaps = 0/4 (0%)

Query 11 LALL 14
 LALL
 Sbjct 8 LALL 11

>gb|AAA54815.1| Sequence 19 from Patent WO 8607383
 Length=22

Score = 17.6 bits (34), Expect = 2.6
 Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 2/12 (16%)

Query 3 VALLPAVLLALL 14
 +AL A+LL LL
 Sbjct 6 IAL--ALLLPLL 15

Score = 15.5 bits (29), Expect = 11
 Identities = 5/6 (83%), Positives = 5/6 (83%), Gaps = 0/6 (0%)

Query 11 LALLAP 16
 LALL P
 Sbjct 8 LALLLP 13

>gb|AAA53695.1| Sequence 2 from Patent WO 9004640
 Length=86

Score = 17.2 bits (33), Expect = 3.5
 Identities = 6/8 (75%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 7 PAVLLALL 14
 PAV+L LL
 Sbjct 3 PAVILFLL 10

>gb|AAA54560.1| Sequence 2 from Patent WO 8805081
 gb|AAA56055.1| Sequence 11 from Patent EP 0273774
 Length=24

Score = 16.8 bits (32), Expect = 4.7
 Identities = 8/13 (61%), Positives = 8/13 (61%), Gaps = 3/13 (23%)

Query 4 ALLPAVLLALLAP 16
 ALL LL LL P
 Sbjct 8 ALL---LLLLLLLP 17

Score = 15.9 bits (30), Expect = 8.5

Identities = 7/11 (63%), Positives = 8/11 (72%), Gaps = 2/11 (18%)

```
Query  4  ALLPAVLLALL  14
        AL  A+ LALL
Sbjct  2  AL--AITLALL  10
```

Score = 15.5 bits (29), Expect = 11
Identities = 7/13 (53%), Positives = 9/13 (69%), Gaps = 2/13 (15%)

```
Query  2  AVALLPAVLLALL  14
        A+ L  A+LL LL
Sbjct  4  AITL--ALLLLLLL  14
```

>gb|AAA54001.1| Sequence 2 from Patent WO 8906283
gb|AAA54156.1| Sequence 42 from Patent WO 8900999
Length=30

Score = 15.9 bits (30), Expect = 8.5
Identities = 7/12 (58%), Positives = 7/12 (58%), Gaps = 3/12 (25%)

```
Query  1  AAVALLPAVLLA  12
        AA  LL  LLA
Sbjct  8  AAAGLL---LLA  16
```

Score = 12.9 bits (23), Expect = 67
Identities = 7/13 (53%), Positives = 7/13 (53%), Gaps = 2/13 (15%)

```
Query  5  LLPAVL--LALLA  15
        LLP      L LLA
Sbjct  4  LLPTAAAGLLLLA  16
```

>gb|AAA00924.1| Sequence 1 from Patent US 4657891
Length=48

Score = 15.9 bits (30), Expect = 8.5
Identities = 8/12 (66%), Positives = 9/12 (75%), Gaps = 0/12 (0%)

```
Query  4  ALLPAVLLALLA  15
        ALL + L ALLA
Sbjct  6  ALLKSKLRALLA  17
```

Database: Protein sequences derived from the Patent division of GenBank
Posted date: Apr 17, 2009 6:11 PM
Number of letters in database: 54,892
Number of sequences in database: 1,417

```
Lambda      K      H
0.335      0.297      1.50
```

Gapped

```
Lambda      K      H
0.294      0.110      0.610
```

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Sequences: 1417

Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 200000: 0
Number of HSP's better than 200000 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 16
Length of database: 54892
Length adjustment: 5
Effective length of query: 11
Effective length of database: 47807
Effective search space: 525877
Effective search space used: 525877
T: 11
A: 40
X1: 1 (0.5 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 1 (3.6 bits)
S2: 0 (3.2 bits)